



SEQUENCE LISTING

<110> Brice, Alexis
Koutnikova, Hana
Fournier, Alain
Pradier, Laurent
Prades, Catherine
Arnould-Reguigne, Isabelle
Rosier-Montus, Marie-Francoise
Corti, Olga

<120> COMPOSITIONS THAT CAN BE USED FOR REGULATING THE ACTIVITY OF PARKIN

<130> ST00005

<140> 09/785,548

<141> 2001-02-20

<160> 50

<170> PatentIn Version 3.2

<210> 1

<211> 1313

<212> DNA

<213> Homo sapiens

<400> 1

cag	aat	ctc	cca	tcc	agt	ccg	gca	ccc	agt	acc	ata	ttc	tct	gga	ggt	48
Gln	Asn	Leu	Pro	Ser	Ser	Pro	Ala	Pro	Ser	Thr	Ile	Phe	Ser	Gly	Gly	
1				5					10					15		

ttt	aga	cac	gga	agt	tta	att	agc	att	gac	agc	acc	tgt	aca	gag	atg	96
Phe	Arg	His	Gly	Ser	Leu	Ile	Ser	Ile	Asp	Ser	Thr	Cys	Thr	Glu	Met	
			20					25					30			

ggc	aat	ttt	gac	aat	gct	aat	gtc	act	gga	gaa	ata	gaa	ttt	gcc	att	144
Gly	Asn	Phe	Asp	Asn	Ala	Asn	Val	Thr	Gly	Glu	Ile	Glu	Phe	Ala	Ile	
		35					40					45				

cat	tat	tgc	ttc	aaa	acc	cat	tct	tta	gaa	ata	tgc	atc	aag	gcc	tgt	192
His	Tyr	Cys	Phe	Lys	Thr	His	Ser	Leu	Glu	Ile	Cys	Ile	Lys	Ala	Cys	
	50					55					60					

aag	aac	ctt	gcc	tat	gga	gaa	gaa	aag	aag	aaa	aag	tgc	aat	ccg	tat	240
Lys	Asn	Leu	Ala	Tyr	Gly	Glu	Glu	Lys	Lys	Lys	Lys	Cys	Asn	Pro	Tyr	
65					70					75					80	

gtg	aag	acc	tac	ctg	ttg	ccc	gac	aga	tcc	tcc	cag	gga	aag	cgc	aag	288
Val	Lys	Thr	Tyr	Leu	Leu	Pro	Asp	Arg	Ser	Ser	Gln	Gly	Lys	Arg	Lys	
				85					90					95		

act	gga	gtc	caa	agg	aac	acc	gtg	gac	ccg	acc	ttt	cag	gag	acc	ttg	336
Thr	Gly	Val	Gln	Arg	Asn	Thr	Val	Asp	Pro	Thr	Phe	Gln	Glu	Thr	Leu	
			100					105					110			

aag	tat	cag	gtg	gcc	cct	gcc	cag	ctg	gtg	acc	cgg	cag	ctg	cag	gtc	384
Lys	Tyr	Gln	Val	Ala	Pro	Ala	Gln	Leu	Val	Thr	Arg	Gln	Leu	Gln	Val	
		115					120					125				

tcg	gtg	tgg	cat	ctg	ggc	acg	ctg	gcc	cgg	aga	gtg	ttt	ctt	gga	gaa	432
Ser	Val	Trp	His	Leu	Gly	Thr	Leu	Ala	Arg	Arg	Val	Phe	Leu	Gly	Glu	
	130					135					140					

gtg atc att tct ctg gcc acg tgg gac ttt gaa gac agc aca aca cag	480
Val Ile Ile Ser Leu Ala Thr Trp Asp Phe Glu Asp Ser Thr Thr Gln	
145 150 155 160	
tcc ttc cgc tgg cat ccg ctc cgg gcc aag gcg gag aaa tac gaa gac	528
Ser Phe Arg Trp His Pro Leu Arg Ala Lys Ala Glu Lys Tyr Glu Asp	
165 170 175	
agc gtt cct cag agt aat gga gag ctc aca gtc cgg gct aag ctg gtt	576
Ser Val Pro Gln Ser Asn Gly Glu Leu Thr Val Arg Ala Lys Leu Val	
180 185 190	
ctc cct tca cgg ccc aga aaa ctc caa gag gct caa gaa ggg aca gat	624
Leu Pro Ser Arg Pro Arg Lys Leu Gln Glu Ala Gln Glu Gly Thr Asp	
195 200 205	
cag cca tca ctt cat ggt caa ctt tgt ttg gta gtg cta gga gcc aag	672
Gln Pro Ser Leu His Gly Gln Leu Cys Leu Val Val Leu Gly Ala Lys	
210 215 220	
aat tta cct gtg cgg cca gat ggc acc ttg aac tca ttt gtt aag ggc	720
Asn Leu Pro Val Arg Pro Asp Gly Thr Leu Asn Ser Phe Val Lys Gly	
225 230 235 240	
tgt ctc act ctg cca gac caa caa aaa ctg aga ctg aag tcg cca gtc	768
Cys Leu Thr Leu Pro Asp Gln Gln Lys Leu Arg Leu Lys Ser Pro Val	
245 250 255	
ctg agg aag cag gct tgc ccc cag tgg aaa cac tca ttt gtc ttc agt	816
Leu Arg Lys Gln Ala Cys Pro Gln Trp Lys His Ser Phe Val Phe Ser	
260 265 270	
ggc gta acc cca gct cag ctg agg cag tcg agc ttg gag tta act gtc	864
Gly Val Thr Pro Ala Gln Leu Arg Gln Ser Ser Leu Glu Leu Thr Val	
275 280 285	
tgg gat cag gcc ctc ttt gga atg aat gac cgc ttg ctt gga gga acc	912
Trp Asp Gln Ala Leu Phe Gly Met Asn Asp Arg Leu Leu Gly Gly Thr	
290 295 300	
aga ctt ggt tca aag gga gac aca gct gtt ggc ggg gat gca tgc tca	960
Arg Leu Gly Ser Lys Gly Asp Thr Ala Val Gly Gly Asp Ala Cys Ser	
305 310 315 320	
cta tcg aag ctc cag tgg cag aaa gtc ctt tcc agc ccc aat cta tgg	1008
Leu Ser Lys Leu Gln Trp Gln Lys Val Leu Ser Ser Pro Asn Leu Trp	
325 330 335	
aca gac atg act ctt gtc ctg cac tgacatgaag gcctcaagggt tccagggttgc	1062
Thr Asp Met Thr Leu Val Leu His	
340	
agcaggcgtg aggcactgtg cgtctgcaga ggggctacga accagggtgca gggtcccagc	1122
tgagagacccc ttgaccttg agcagtcctcc atctgcggcc ctgtcccatg gcttaaccgc	1182
ctattggtat ctgtgtatat ttacgttaaa cacaattatg ttacctaagc ctctggtggg	1242
ttatctcctc ttgagatgt agaaaatggc cagattttaa taaacgttgt tacccatgaa	1302
aaaaaaaaa a	1313

<211> 344
 <212> PRT
 <213> Homo sapiens

<400> 2

Gln Asn Leu Pro Ser Ser Pro Ala Pro Ser Thr Ile Phe Ser Gly Gly
 1 5 10 15
 Phe Arg His Gly Ser Leu Ile Ser Ile Asp Ser Thr Cys Thr Glu Met
 20 25 30
 Gly Asn Phe Asp Asn Ala Asn Val Thr Gly Glu Ile Glu Phe Ala Ile
 35 40 45
 His Tyr Cys Phe Lys Thr His Ser Leu Glu Ile Cys Ile Lys Ala Cys
 50 55 60
 Lys Asn Leu Ala Tyr Gly Glu Glu Lys Lys Lys Lys Cys Asn Pro Tyr
 65 70 75 80
 Val Lys Thr Tyr Leu Leu Pro Asp Arg Ser Ser Gln Gly Lys Arg Lys
 85 90 95
 Thr Gly Val Gln Arg Asn Thr Val Asp Pro Thr Phe Gln Glu Thr Leu
 100 105 110
 Lys Tyr Gln Val Ala Pro Ala Gln Leu Val Thr Arg Gln Leu Gln Val
 115 120 125
 Ser Val Trp His Leu Gly Thr Leu Ala Arg Arg Val Phe Leu Gly Glu
 130 135 140
 Val Ile Ile Ser Leu Ala Thr Trp Asp Phe Glu Asp Ser Thr Thr Gln
 145 150 155 160
 Ser Phe Arg Trp His Pro Leu Arg Ala Lys Ala Glu Lys Tyr Glu Asp
 165 170 175
 Ser Val Pro Gln Ser Asn Gly Glu Leu Thr Val Arg Ala Lys Leu Val
 180 185 190
 Leu Pro Ser Arg Pro Arg Lys Leu Gln Glu Ala Gln Glu Gly Thr Asp
 195 200 205
 Gln Pro Ser Leu His Gly Gln Leu Cys Leu Val Val Leu Gly Ala Lys
 210 215 220
 Asn Leu Pro Val Arg Pro Asp Gly Thr Leu Asn Ser Phe Val Lys Gly
 225 230 235 240
 Cys Leu Thr Leu Pro Asp Gln Gln Lys Leu Arg Leu Lys Ser Pro Val
 245 250 255
 Leu Arg Lys Gln Ala Cys Pro Gln Trp Lys His Ser Phe Val Phe Ser
 260 265 270
 Gly Val Thr Pro Ala Gln Leu Arg Gln Ser Ser Leu Glu Leu Thr Val
 275 280 285
 Trp Asp Gln Ala Leu Phe Gly Met Asn Asp Arg Leu Leu Gly Gly Thr
 290 295 300
 Arg Leu Gly Ser Lys Gly Asp Thr Ala Val Gly Gly Asp Ala Cys Ser
 305 310 315 320

Leu Ser Lys Leu Gln Trp Gln Lys Val Leu Ser Ser Pro Asn Leu Trp
 325 330 335

Thr Asp Met Thr Leu Val Leu His
 340

<210> 3
 <211> 471
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(471)

<400> 3
 gga agt cca gca ggt aga tca atc tac aac agc ttt tat gtg tat tgc 48
 Gly Ser Pro Ala Gly Arg Ser Ile Tyr Asn Ser Phe Tyr Val Tyr Cys
 1 5 10 15
 aaa ggc ccc tgt caa aga gtg cag ccg gga aaa ctc agg gta cag tgc 96
 Lys Gly Pro Cys Gln Arg Val Gln Pro Gly Lys Leu Arg Val Gln Cys
 20 25 30
 agc acc tgc agg cag gca acg ctc acc ttg acc cag ggt cca tct tgc 144
 Ser Thr Cys Arg Gln Ala Thr Leu Thr Gln Gly Pro Ser Cys
 35 40 45
 tgg gat gat gtt tta att cca aac cgg atg agt ggt gaa tgc caa tcc 192
 Trp Asp Asp Val Leu Ile Pro Asn Arg Met Ser Gly Glu Cys Gln Ser
 50 55 60
 cca cac tgc cct ggg act agt gca gaa ttt ttc ttt aaa tgt gga gca 240
 Pro His Cys Pro Gly Thr Ser Ala Glu Phe Phe Phe Lys Cys Gly Ala
 65 70 75 80
 cac ccc acc tct gac aag gaa aca tca gta gct ttg cac ctg atc gca 288
 His Pro Thr Ser Asp Lys Glu Thr Ser Val Ala Leu His Leu Ile Ala
 85 90 95
 aca aat agt cgg aac atc act tgc att acg tgc aca gac gtc agg agc 336
 Thr Asn Ser Arg Asn Ile Thr Cys Ile Thr Cys Thr Asp Val Arg Ser
 100 105 110
 ccc gtc ctg gtt ttc cag tgc aac tcc cgc cac gtg att tgc tta gac 384
 Pro Val Leu Val Phe Gln Cys Asn Ser Arg His Val Ile Cys Leu Asp
 115 120 125
 tgt ttc cac tta tac tgt gtg aca aga ctc aat gat cgg cag ttt gtt 432
 Cys Phe His Leu Tyr Cys Val Thr Arg Leu Asn Asp Arg Gln Phe Val
 130 135 140
 cac gac cct caa ctt ggc tac tcc ctg cct tgt gtg tag 471
 His Asp Pro Gln Leu Gly Tyr Ser Leu Pro Cys Val
 145 150 155

<210> 4
 <211> 156
 <212> PRT
 <213> Homo sapiens

<400> 4
 Gly Ser Pro Ala Gly Arg Ser Ile Tyr Asn Ser Phe Tyr Val Tyr Cys
 1 5 10 15
 Lys Gly Pro Cys Gln Arg Val Gln Pro Gly Lys Leu Arg Val Gln Cys
 20 25 30
 Ser Thr Cys Arg Gln Ala Thr Leu Thr Leu Thr Gln Gly Pro Ser Cys
 35 40 45
 Trp Asp Asp Val Leu Ile Pro Asn Arg Met Ser Gly Glu Cys Gln Ser
 50 55 60
 Pro His Cys Pro Gly Thr Ser Ala Glu Phe Phe Phe Lys Cys Gly Ala
 65 70 75 80
 His Pro Thr Ser Asp Lys Glu Thr Ser Val Ala Leu His Leu Ile Ala
 85 90 95
 Thr Asn Ser Arg Asn Ile Thr Cys Ile Thr Cys Thr Asp Val Arg Ser
 100 105 110
 Pro Val Leu Val Phe Gln Cys Asn Ser Arg His Val Ile Cys Leu Asp
 115 120 125
 Cys Phe His Leu Tyr Cys Val Thr Arg Leu Asn Asp Arg Gln Phe Val
 130 135 140
 His Asp Pro Gln Leu Gly Tyr Ser Leu Pro Cys Val
 145 150 155

<210> 5
 <211> 27
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence:Oligonucleotide

<400> 5
 ttaagaattc ggaagtccag caggtag 27

<210> 6
 <211> 29
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence:Oligonucleotide

<400> 6
 attagatcc ctacacaaa ggcagggag 29

<210> 7
 <211> 19
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence:Oligonucleotide

<400> 7
 gcgtttggaa tcactacag 19

<210> 8
 <211> 17
 <212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:Oligonucleotide

<400> 8

ggtctcggtg tggcatc

17

<210> 9

<211> 18

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:Oligonucleotide

<400> 9

ccgcttgctt ggaggaac

18

<210> 10

<211> 18

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:Oligonucleotide

<400> 10

cgtatttctc cgccttgg

18

<210> 11

<211> 28

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:Oligonucleotide

<400> 11

aatagctcga gtcagtgacg gacaagag

28

<210> 12

<211> 2347

<212> DNA

<213> Homo sapiens

<400> 12

ggccttgggg	cactgagggg	tgccagttct	gcctgttcat	ctggaacctg	gatctaagga	60
gggaagaggc	gttgcccctg	ctggcatagt	caggtaccag	cccagccagg	tattgaacgg	120
gctgagcttt	tcagtatggt	tcctgctgac	ctggaaacat	cttaaattga	agggcgtgag	180
cgcttgggtc	atgcagtga	gctcttccaa	cctgggtcaa	cgaaaacgga	gaagaaatgg	240
cccaagaaat	agatctgagt	gctctcaagg	agttagaacg	cgaggccatt	ctccaggtcc	300
tgtaccgaga	ccaggcgggt	caaaacacag	aggaggagag	gacacggaaa	ctgaaaacac	360
acctgcagca	tctccgggtg	aaaggagcga	agaacacgga	ctgggagcac	aaagagaagt	420
gctgtgcgcg	ctgccagcag	gtgctggggt	tcctgctgca	ccggggcgcc	gtgtgccggg	480
gctgcagcca	ccgcgtgtgt	gcccagtgcc	gagtgttcct	gagggggacc	catgcctgga	540
agtgcacggt	gtgcttcgag	gacaggaatg	tcaaaataaa	aactggagaa	tggttctatg	600
aggaacgagc	caagaaattt	ccaactggag	gcaaacatga	gacagttgga	gggcagctct	660
tgcaatctta	tcagaagctg	agcaaaattt	ctgtggttcc	tcctactcca	cctcctgtca	720
gcgagagcca	gtgcagccgc	agtcctggca	ggttacagga	atttggtcag	tttagaggat	780

```

ttaataagtc cgtggaaaat ttgtttctgt ctcttgctac ccacgtgaaa aagctctcca 840
aatcccagaa tgatatgact tctgagaagc atcttctcgc cacgggcccc aggcagtgtg 900
tgggacagac agagagacgg agccagtctg acactgcggt caacgtcacc accaggaagg 960
tcagtgcacc agatattctg aaacctctca atcaagagga tcccaaatgc tctactaacc 1020
ctattttgaa gcaacagaat ctcccatcca gtccggcacc cagtaccata ttctctggag 1080
gttttagaca cggaagttaa attagcattg acagcacctg tacagagatg ggcaattttg 1140
acaatgctaa tgtcactgga gaaatagaat ttgccattca ttattgcttc aaaaccatt 1200
ctttagaaat atgcatcaag gcctgtaaga acctgccta tggagaagaa aagaagaaaa 1260
agtgcaatcc gtatgtgaag acctacctgt tgcccgcag atcctcccag ggaaagcgca 1320
agactggagt ccaaaggaac accgtggacc cgacctttca ggagaccttg aagtatcagg 1380
tggccccctgc ccagctgggtg acccggcagc tgcaggtctc ggtgtggcat ctgggcacgc 1440
tggccccggag agtgtttctt ggagaagtga tcattcctct ggccacgtgg gactttgaag 1500
acagcacaac acagtccttc cgctggcatc cgctccgggc caaggcggag aaatacgaag 1560
acagcgttcc tcagagtaat ggagagctca cagtccgggc taagctggtt ctcccttcac 1620
ggcccagaaa actccaagag gctcaagaag ggacagatca gccatcactt catggtcaac 1680
tttgtttggt agtgctagga gccaaagaat tacctgtgcg gccagatggc accttgaact 1740
catttgtaa gggctgtctc actctgccag accaacaata actgagactg aagtcgccag 1800
tcctgaggaa cccagcttgc cccagtgga aacactcatt tgtcttcagt ggcgtaacc 1860
cagctcagct gaggcagtcg agcttgaggt taactgtctg ggatcaggcc ctctttggaa 1920
tgaacgaccg cttgcttgga ggaaccagac ttggttcaaa gggagacaca gctgttggcg 1980
gggatgcatg ctcacaatcg aagctccagt ggcagaaagt cctttccagc cccaatctat 2040
ggacagacat gactcttgct ctgcactgac atgaaggcct caaggttcca ggttgagca 2100
ggcgtgaggc actgtgcgtc tgcagagggg ctacgaacca ggtgcagggt cccagctgga 2160
gacctctttg accttgagca gtctccatct gcggccctgt cccatggctt aaccgcctat 2220
tggatatctg gtatatttac gttaaacaca attatgttac ctaagcctct ggtgggttat 2280
ctcctctttg agatgtagaa aatggccaga ttttaataaa cgttggtacc catgaaaaaa 2340
aaaaaaa

```

<210> 13
 <211> 610
 <212> PRT
 <213> Homo sapiens

<400> 13
 Met Ala Gln Glu Ile Asp Leu Ser Ala Leu Lys Glu Leu Glu Arg Glu
 1 5 10 15
 Ala Ile Leu Gln Val Leu Tyr Arg Asp Gln Ala Val Gln Asn Thr Glu
 20 25 30
 Glu Glu Arg Thr Arg Lys Leu Lys Thr His Leu Gln His Leu Arg Trp
 35 40 45
 Lys Gly Ala Lys Asn Thr Asp Trp Glu His Lys Glu Lys Cys Cys Ala
 50 55 60
 Arg Cys Gln Gln Val Leu Gly Phe Leu Leu His Arg Gly Ala Val Cys
 65 70 75 80
 Arg Gly Cys Ser His Arg Val Cys Ala Gln Cys Arg Val Phe Leu Arg
 85 90 95
 Gly Thr His Ala Trp Lys Cys Thr Val Cys Phe Glu Asp Arg Asn Val
 100 105 110
 Lys Ile Lys Thr Gly Glu Trp Phe Tyr Glu Glu Arg Ala Lys Lys Phe
 115 120 125
 Pro Thr Gly Gly Lys His Glu Thr Val Gly Gly Gln Leu Leu Gln Ser
 130 135 140
 Tyr Gln Lys Leu Ser Lys Ile Ser Val Val Pro Thr Pro Pro Pro
 145 150 155 160
 Page 7

Val Ser Glu Ser Gln Cys Ser Arg Ser Pro Gly Arg Leu Gln Glu Phe
165 170 175
Gly Gln Phe Arg Gly Phe Asn Lys Ser Val Glu Asn Leu Phe Leu Ser
180 185 190
Leu Ala Thr His Val Lys Lys Leu Ser Lys Ser Gln Asn Asp Met Thr
195 200 205
Ser Glu Lys His Leu Leu Ala Thr Gly Pro Arg Gln Cys Val Gly Gln
210 215 220
Thr Glu Arg Arg Ser Gln Ser Asp Thr Ala Val Asn Val Thr Thr Arg
225 230 235 240
Lys Val Ser Ala Pro Asp Ile Leu Lys Pro Leu Asn Gln Glu Asp Pro
245 250 255
Lys Cys Ser Thr Asn Pro Ile Leu Lys Gln Gln Asn Leu Pro Ser Ser
260 265 270
Pro Ala Pro Ser Thr Ile Phe Ser Gly Gly Phe Arg His Gly Ser Leu
275 280 285
Ile Ser Ile Asp Ser Thr Cys Thr Glu Met Gly Asn Phe Asp Asn Ala
290 295 300
Asn Val Thr Gly Glu Ile Glu Phe Ala Ile His Tyr Cys Phe Lys Thr
305 310 315 320
His Ser Leu Glu Ile Cys Ile Lys Ala Cys Lys Asn Leu Ala Tyr Gly
325 330 335
Glu Glu Lys Lys Lys Lys Cys Asn Pro Tyr Val Lys Thr Tyr Leu Leu
340 345 350
Pro Asp Arg Ser Ser Gln Gly Lys Arg Lys Thr Gly Val Gln Arg Asn
355 360 365
Thr Val Asp Pro Thr Phe Gln Glu Thr Leu Lys Tyr Gln Val Ala Pro
370 375 380
Ala Gln Leu Val Thr Arg Gln Leu Gln Val Ser Val Trp His Leu Gly
385 390 395 400
Thr Leu Ala Arg Arg Val Phe Leu Gly Glu Val Ile Ile Pro Leu Ala
405 410 415
Thr Trp Asp Phe Glu Asp Ser Thr Thr Gln Ser Phe Arg Trp His Pro
420 425 430
Leu Arg Ala Lys Ala Glu Lys Tyr Glu Asp Ser Val Pro Gln Ser Asn
435 440 445
Gly Glu Leu Thr Val Arg Ala Lys Leu Val Leu Pro Ser Arg Pro Arg
450 455 460
Lys Leu Gln Glu Ala Gln Glu Gly Thr Asp Gln Pro Ser Leu His Gly
465 470 475 480
Gln Leu Cys Leu Val Val Leu Gly Ala Lys Asn Leu Pro Val Arg Pro
485 490 495

Asp Gly Thr Leu Asn Ser Phe Val Lys Gly Cys Leu Thr Leu Pro Asp
 500 505 510
 Gln Gln Lys Leu Arg Leu Lys Ser Pro Val Leu Arg Lys Gln Ala Cys
 515 520 525
 Pro Gln Trp Lys His Ser Phe Val Phe Ser Gly Val Thr Pro Ala Gln
 530 535 540
 Leu Arg Gln Ser Ser Leu Glu Leu Thr Val Trp Asp Gln Ala Leu Phe
 545 550 555 560
 Gly Met Asn Asp Arg Leu Leu Gly Gly Thr Arg Leu Gly Ser Lys Gly
 565 570 575
 Asp Thr Ala Val Gly Gly Asp Ala Cys Ser Gln Ser Lys Leu Gln Trp
 580 585 590
 Gln Lys Val Leu Ser Ser Pro Asn Leu Trp Thr Asp Met Thr Leu Val
 595 600 605
 Leu His
 610

<210> 14
 <211> 1648
 <212> DNA
 <213> Homo sapiens

<400> 14
 gaaatcatgc ccctcgtaga gcagcaggtc caagcagggc tgctggctat ttttccaaaa 60
 agtgaggcag tttaaaaaaa aggcggagaa ctagaattat agaataatgg cacatattgt 120
 gtatttgtaa aactaacggc ttgcatgggt cacaacccat ttcttatgcc tgtgttttcc 180
 ttggcagcaa aatttctgtg gttcctccta ctccacctcc tgtcagcgag agccagtgc 240
 gccgcagtcc tggcaggaag gtcagtgcac cagatattct gaaacctctc aatcaagagg 300
 atcccaaagt ctctactaac cctattttga agcaacagaa tctcccatcc agtccggcac 360
 ccagtacat attctctgga ggtttttagac acggaagttt aattagcatt gacagcacct 420
 gtacagagat gggcaatttt gacaatgcta atgtcactgg agaaatagaa tttgccattc 480
 attattgctt caaaacccat tctttagaaa tatgcatcaa ggcctgtaag aaccttgctt 540
 atggagaaga aaagaagaaa aagtgaatc cgtatgtgaa gacctacctg ttgcccga 600
 gatcctccca gggaaagcgc aagactggag tccaaaggaa caccgtggac ccgacctttc 660
 aggagacctt gaagtatcag gtggcccctg cccagctggg gacccggcag ctgcaggtct 720
 cgggtgtggc tctgggcacg ctggcccgga gagtgtttct tggagaagtg atcattcctc 780
 tggccacgtg ggactttgaa gacagcacia cacagtcctt ccgctggcat ccgctccggg 840
 ccaaggcgga gaaatacgaa gacagcggtc ctacagagtaa tggagagctc acagtccggg 900
 ctaagctggt tctcccttca cggcccagaa aactccaaga ggctcaagaa gggacagatc 960
 agccatcact tcatggtcaa ctttgtttgg tagtgctagg agccaagaat ttacctgtgc 1020
 ggccagatgg caccttgaac tcatttgtaa agggctgtct cactctgcca gaccaaaaa 1080
 aactgagact gaagtgcga gtccctgagg agcaggcttg ccccagtgag aaacactcat 1140
 ttgtcttcag tggcgtaacc ccagctcagc tgaggcagtc gagcttgagg ttaactgtct 1200
 gggatcaggc cctctttgga atgaacgacc gcttgcttgg aggaaccaga cttggttcaa 1260
 agggagacac agctgttggc ggggatgcat gctcacaatc gaagctccag tggcagaag 1320
 tcctttccag cccaatcta tggacagaca tgactcttgt cctgcactga catgaaggcc 1380
 tcaaggttcc aggttgagc aggcgtgagg cactgtgcgt ctgcagaggg gctacgaacc 1440
 aggtgcaggg tcccagctgg agaccccttt gaccttgagc agtctccatc tgcggccctg 1500
 tcccatggct taaccgccta ttggtatctg tgtatattta cgttaaacac aattatgtta 1560
 cctaagctc tgggtgggta tctcctcttt gagatgtaga aaatggccag attttaataa 1620
 acgttggtac ccatgaaaaa aaaaaaaa 1648

<210> 15
 <211> 313
 <212> PRT

<213> Homo sapiens

<400> 15

Met Gly Asn Phe Asp Asn Ala Asn Val Thr Gly Glu Ile Glu Phe Ala
1 5 10 15
Ile His Tyr Cys Phe Lys Thr His Ser Leu Glu Ile Cys Ile Lys Ala
20 25 30
Cys Lys Asn Leu Ala Tyr Gly Glu Glu Lys Lys Lys Lys Cys Asn Pro
35 40 45
Tyr Val Lys Thr Tyr Leu Leu Pro Asp Arg Ser Ser Gln Gly Lys Arg
50 55 60
Lys Thr Gly Val Gln Arg Asn Thr Val Asp Pro Thr Phe Gln Glu Thr
65 70 75 80
Leu Lys Tyr Gln Val Ala Pro Ala Gln Leu Val Thr Arg Gln Leu Gln
85 90 95
Val Ser Val Trp His Leu Gly Thr Leu Ala Arg Arg Val Phe Leu Gly
100 105 110
Glu Val Ile Ile Pro Leu Ala Thr Trp Asp Phe Glu Asp Ser Thr Thr
115 120 125
Gln Ser Phe Arg Trp His Pro Leu Arg Ala Lys Ala Glu Lys Tyr Glu
130 135 140
Asp Ser Val Pro Gln Ser Asn Gly Glu Leu Thr Val Arg Ala Lys Leu
145 150 155 160
Val Leu Pro Ser Arg Pro Arg Lys Leu Gln Glu Ala Gln Glu Gly Thr
165 170 175
Asp Gln Pro Ser Leu His Gly Gln Leu Cys Leu Val Val Leu Gly Ala
180 185 190
Lys Asn Leu Pro Val Arg Pro Asp Gly Thr Leu Asn Ser Phe Val Lys
195 200 205
Gly Cys Leu Thr Leu Pro Asp Gln Gln Lys Leu Arg Leu Lys Ser Pro
210 215 220
Val Leu Arg Lys Gln Ala Cys Pro Gln Trp Lys His Ser Phe Val Phe
225 230 235 240
Ser Gly Val Thr Pro Ala Gln Leu Arg Gln Ser Ser Leu Glu Leu Thr
245 250 255
Val Trp Asp Gln Ala Leu Phe Gly Met Asn Asp Arg Leu Leu Gly Gly
260 265 270
Thr Arg Leu Gly Ser Lys Gly Asp Thr Ala Val Gly Gly Asp Ala Cys
275 280 285
Ser Gln Ser Lys Leu Gln Trp Gln Lys Val Leu Ser Ser Pro Asn Leu
290 295 300
Trp Thr Asp Met Thr Leu Val Leu His
305 310

<210> 16
 <211> 19
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Description of the artificial sequence:oligonucleotide

 <400> 16
 ccagttctgc ctgttcac 19

<210> 17
 <211> 20
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Description of the artificial sequence:oligonucleotide

 <400> 17
 ttcaaaacac agaggaggag 20

<210> 18
 <211> 20
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Description of the artificial sequence:oligonucleotide

 <400> 18
 gaatttggtc agtttagagg 20

<210> 19
 <211> 26
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Description of the artificial sequence:oligonucleotide

 <400> 19
 ttctgggatt tggagagctt tttcac 26

<210> 20
 <211> 22
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Description of the artificial sequence:oligonucleotide

 <400> 20
 tctgtctgtc ccacacactg cc 22

<210> 21
 <211> 19
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence:oligonucleotide
 <400> 21
 gactggctcc gtctctctg 19

<210> 22
 <211> 21
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence:oligonucleotide
 <400> 22
 aagcaacaga atctcccatc c 21

<210> 23
 <211> 21
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence:oligonucleotide
 <400> 23
 gcattgtcaa aattgcccat c 21

<210> 24
 <211> 20
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence:oligonucleotide
 <400> 24
 aggcggagaa atacgaagac 20

<210> 25
 <211> 22
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence:oligonucleotide
 <400> 25
 gcagagtgag acagccctta ac 22

<210> 26
 <211> 24
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence:oligonucleotide

<400> 26
 cttcctcagg actggcgact tcag 24

<210> 27
 <211> 24
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence:oligonucleotide

<400> 27
 caagcggtcg ttcattccaa agag 24

<210> 28
 <211> 22
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence:oligonucleotide

<400> 28
 aagaggagat aaccaccag ag 22

<210> 29
 <211> 20
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence:oligonucleotide

<400> 29
 agggctgctg gctatatttc 20

<210> 30
 <211> 19
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence:oligonucleotide

<400> 30
 taagaaatgg gttgtgaac 19

<210> 31
 <211> 21
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence:oligonucleotide

<400> 31
 aagcaacaga atctcccatc c 21

<210> 32
 <211> 21
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Description of the artificial sequence:oligonucleotide

 <400> 32
 gcattgtcaa aattgcccat c 21

<210> 33
 <211> 20
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Description of the artificial sequence:oligonucleotide

 <400> 33
 aggcggagaa atacgaagac 20

<210> 34
 <211> 22
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Description of the artificial sequence:oligonucleotide

 <400> 34
 gcagagtgag acagccctta ac 22

<210> 35
 <211> 24
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Description of the artificial sequence:oligonucleotide

 <400> 35
 cttcctcagg actggcgact tcag 24

<210> 36
 <211> 24
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Description of the artificial sequence:oligonucleotide

 <400> 36
 caagcggtcg ttcattccaa agag 24

<210> 37
 <211> 22
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence:oligonucleotide
 <400> 37
 aagaggagat aaccaccag ag 22

<210> 38
 <211> 18
 <212> DNA
 <213> Artificial sequence
 <220>
 <223> Description of the artificial sequence:oligonucleotide
 <400> 38
 aatggaaggg cgtgacgc 18

<210> 39
 <211> 21
 <212> DNA
 <213> Artificial sequence
 <220>
 <223> Description of the artificial sequence:oligonucleotide
 <400> 39
 cctcacgcct gctgcaacct g 21

<210> 40
 <211> 31
 <212> DNA
 <213> Artificial sequence
 <220>
 <223> Description of the artificial sequence:oligonucleotide
 <400> 40
 gcacgaattc atggcccaag aaatagatct g 31

<210> 41
 <211> 24
 <212> DNA
 <213> Artificial sequence
 <220>
 <223> Description of the artificial sequence:oligonucleotide
 <400> 41
 ctgtcttcgt atttctccgc cttg 24

<210> 42
 <211> 2347
 <212> DNA
 <213> Homo sapiens
 <220>
 <223> Delete: this sequence is a duplicate of Sequence 12

```

<400> 42
ggccttgggg cactgagggg tgccagttct gcctgttcat ctggaacctg gatctaagga 60
gggaagaggc gttgcccctg ctggcatagt caggtagcag cccagccagg tattgaacgg 120
gctgagcttt tcatgatggt tcctgctgac ctggaacat cttaaagga agggcgtgag 180
cgcttggtcc atgcagtga gctcttccaa cctgggtcaa cgaaaacgga gaagaaatgg 240
cccaagaaat agatctgagt gctctcaagg agttaagaac cgaggccatt ctccaggtcc 300
tgtaccgaga ccaggcgggt caaaacacag aggaggagag gacacggaaa ctgaaaacac 360
acctgcagca tctccggtgg aaaggagcga agaacacgga ctgggagcac aaagagaagt 420
gctgtgcgcg ctgccagcag gtgctggggg tcctgctgca ccggggcgcc gtgtgccggg 480
gctgcagcca ccgctgtgtg gccagtgcc gagtgttctt gagggggacc catgcctgga 540
agtgcacggg gtgcttcgag gacaggaatg tcaaaataaa aactggagaa tggttctatg 600
aggaacgagc caagaaatct ccaactggag gcaaacaatga gacagttgga gggcagctct 660
tgcaatctta tcagaagctg agcaaaatct ctgtggttcc tcctactcca cctcctgtca 720
gagagagcca gtgcagccgc agtcctggca ggtagcagga atttggtcag tttagaggat 780
ttaataagtc cgtggaaaat ttgtttctgt ctcttgctac ccacgtgaaa aagctctcca 840
aatcccagaa tgatatgact tctgagaagc atcttctcgc cacgggcccc aggcagtgtg 900
tgggacagaa agagagacgg agccagtctg acactgcggg caacgtcacc accaggaagg 960
tcagtgcacc agatattctg aaacctctca atcaagagga tcccaaatgc tctactaacc 1020
ctattttgaa gcaacagaat ctcccatcca gtccggcacc cagtaccata ttctctggag 1080
gttttagaca cggaagttaa attagcattg acagcacctg tacagagatg ggcaattttg 1140
acaatgctaa tgtcactgga gaaatagaat ttgccattca ttattgcttc aaaaccctt 1200
ctttagaagt atgcatcaag gcctgtaaga acctgtcctg tgcccagacag atcctcccag ggaaagcgca 1320
agtgaatccc gtagtgtaag acctacctgt tgcccagacag atcctcccag ggaaagcgca 1380
agactggagt ccaaaggaac accgtggacc cgacctttca ggagaccttg aagtatcagg 1440
tgccccctgc ccagctggtg acccggcagc tgcaggtctc ggtgtggcat ctgggcacgc 1500
tgccccggag agtgtttctt ggagaagtga tcattcctct ggccacgtgg gactttgaag 1560
acagcacaac acagtccttc cgctggcatc cgctccgggc caaggcggag aaatacgaag 1620
acagcgttcc tcagagtaat ggagagctca cagtccgggc taagctggtt ctcccttcac 1680
ggcccagaaa actccaagag gctcaagaag ggacagatca gccatcactt catggtcaac 1740
tttgtttggt agtgctagga gccaagaatt tacctgtgcg gccagatggc acctggaact 1800
catttgttaa gggctgtctc actctgccag accaacaata actgagactg aagtcgccag 1860
tcctgaggaa gcaggcttgc cccagtgga aacactcatt tgtcttcagt ggcgtaaccc 1920
cagctcagct gaggcagtcg agcttgaggt taactgtctg ggatcaggcc ctctttggaa 1980
tgaacgaccg cttgcttggg ggaaccagac ttggttcaaa gggagacaca gctgttggcg 2040
gggatgcatg ctcaaatcg aagctccagt ggcagaaagt cctttccagc cccaatctat 2100
ggacagacat gactcttgtc ctgactgac atgaaggcct caaggttcca ggttgagca 2160
ggcgtgaggc actgtgcgtc tgcagagggg ctacgaacca ggtgcagggt cccagctgga 2220
gacccctttg accttgagca gtctccatct gcggccctgt cccatggctt aaccgcctat 2280
tggtatctgt gtatatattac gttaaacaca attatgttac ctaagcctct ggtgggttat 2340
ctcctctttg agatgtagaa aatggccaga ttttaataaa cgttggttacc catgaaaaaa 2347
aaaaaa

```

```

<210> 43
<211> 610
<212> PRT
<213> Homo sapiens

```

```

<220>
<223> Delete: this sequence is a duplicate of Sequence 13

```

```

<400> 43
Met Ala Gln Glu Ile Asp Leu Ser Ala Leu Lys Glu Leu Glu Arg Glu
 1             5             10             15

Ala Ile Leu Gln Val Leu Tyr Arg Asp Gln Ala Val Gln Asn Thr Glu
      20             25             30

Glu Glu Arg Thr Arg Lys Leu Lys Thr His Leu Gln His Leu Arg Trp
 35             40             45

Lys Gly Ala Lys Asn Thr Asp Trp Glu His Lys Glu Lys Cys Cys Ala
 50             55             60

```


Arg Cys Gln Gln Val Leu Gly Phe Leu Leu His Arg Gly Ala Val Cys
 65 70 75 80
 Arg Gly Cys Ser His Arg Val Cys Ala Gln Cys Arg Val Phe Leu Arg
 85 90 95
 Gly Thr His Ala Trp Lys Cys Thr Val Cys Phe Glu Asp Arg Asn Val
 100 105 110
 Lys Ile Lys Thr Gly Glu Trp Phe Tyr Glu Glu Arg Ala Lys Lys Phe
 115 120 125
 Pro Thr Gly Gly Lys His Glu Thr Val Gly Gly Gln Leu Leu Gln Ser
 130 135 140
 Tyr Gln Lys Leu Ser Lys Ile Ser Val Val Pro Pro Thr Pro Pro Pro
 145 150 155 160
 Val Ser Glu Ser Gln Cys Ser Arg Ser Pro Gly Arg Leu Gln Glu Phe
 165 170 175
 Gly Gln Phe Arg Gly Phe Asn Lys Ser Val Glu Asn Leu Phe Leu Ser
 180 185 190
 Leu Ala Thr His Val Lys Lys Leu Ser Lys Ser Gln Asn Asp Met Thr
 195 200 205
 Ser Glu Lys His Leu Leu Ala Thr Gly Pro Arg Gln Cys Val Gly Gln
 210 215 220
 Thr Glu Arg Arg Ser Gln Ser Asp Thr Ala Val Asn Val Thr Thr Arg
 225 230 235 240
 Lys Val Ser Ala Pro Asp Ile Leu Lys Pro Leu Asn Gln Glu Asp Pro
 245 250 255
 Lys Cys Ser Thr Asn Pro Ile Leu Lys Gln Gln Asn Leu Pro Ser Ser
 260 265 270
 Pro Ala Pro Ser Thr Ile Phe Ser Gly Gly Phe Arg His Gly Ser Leu
 275 280 285
 Ile Ser Ile Asp Ser Thr Cys Thr Glu Met Gly Asn Phe Asp Asn Ala
 290 295 300
 Asn Val Thr Gly Glu Ile Glu Phe Ala Ile His Tyr Cys Phe Lys Thr
 305 310 315 320
 His Ser Leu Glu Ile Cys Ile Lys Ala Cys Lys Asn Leu Ala Tyr Gly
 325 330 335
 Glu Glu Lys Lys Lys Lys Cys Asn Pro Tyr Val Lys Thr Tyr Leu Leu
 340 345 350
 Pro Asp Arg Ser Ser Gln Gly Lys Arg Lys Thr Gly Val Gln Arg Asn
 355 360 365
 Thr Val Asp Pro Thr Phe Gln Glu Thr Leu Lys Tyr Gln Val Ala Pro
 370 375 380
 Ala Gln Leu Val Thr Arg Gln Leu Gln Val Ser Val Trp His Leu Gly
 385 390 395 400
 Thr Leu Ala Arg Arg Val Phe Leu Gly Glu Val Ile Ile Pro Leu Ala

				405						410						415			
Thr	Trp	Asp	Phe	Glu	Asp	Ser	Thr	Thr	Gln	Ser	Phe	Arg	Trp	His	Pro				
			420					425					430						
Leu	Arg	Ala	Lys	Ala	Glu	Lys	Tyr	Glu	Asp	Ser	Val	Pro	Gln	Ser	Asn				
		435					440					445							
Gly	Glu	Leu	Thr	Val	Arg	Ala	Lys	Leu	Val	Leu	Pro	Ser	Arg	Pro	Arg				
	450					455					460								
Lys	Leu	Gln	Glu	Ala	Gln	Glu	Gly	Thr	Asp	Gln	Pro	Ser	Leu	His	Gly				
465					470					475					480				
Gln	Leu	Cys	Leu	Val	Val	Leu	Gly	Ala	Lys	Asn	Leu	Pro	Val	Arg	Pro				
			485						490					495					
Asp	Gly	Thr	Leu	Asn	Ser	Phe	Val	Lys	Gly	Cys	Leu	Thr	Leu	Pro	Asp				
			500					505					510						
Gln	Gln	Lys	Leu	Arg	Leu	Lys	Ser	Pro	Val	Leu	Arg	Lys	Gln	Ala	Cys				
		515					520					525							
Pro	Gln	Trp	Lys	His	Ser	Phe	Val	Phe	Ser	Gly	Val	Thr	Pro	Ala	Gln				
	530					535					540								
Leu	Arg	Gln	Ser	Ser	Leu	Glu	Leu	Thr	Val	Trp	Asp	Gln	Ala	Leu	Phe				
545					550					555					560				
Gly	Met	Asn	Asp	Arg	Leu	Leu	Gly	Gly	Thr	Arg	Leu	Gly	Ser	Lys	Gly				
				565					570					575					
Asp	Thr	Ala	Val	Gly	Gly	Asp	Ala	Cys	Ser	Gln	Ser	Lys	Leu	Gln	Trp				
			580					585					590						
Gln	Lys	Val	Leu	Ser	Ser	Pro	Asn	Leu	Trp	Thr	Asp	Met	Thr	Leu	Val				
		595					600					605							
Leu	His																		
	610																		

<210> 44
 <211> 1648
 <212> DNA
 <213> Homo sapiens

<220>
 <223> Delete: this sequence is a duplicate of Sequence 14

<400> 44

gaaatcatgc	ccctcgtaga	gcagcaggtc	caagcagggc	tgctggctat	ttttccaaaa	60
agtgaggcag	tttaaaaaaa	aggcggagaa	ctagaattat	agaataatgg	cacattttgt	120
gtatttgtaa	aactaacggc	ttgcatgggt	cacaacccat	ttcttatgcc	tgtgttttcc	180
ttggcagcaa	aattttctgtg	gttcttccta	ctccacctcc	tgtcagcgag	agccagtgc	240
gccgcagtcc	tggcaggaag	gtcagtgcac	cagatattct	gaaacctctc	aatcaagagg	300
atcccaaattg	ctctactaac	cctattttga	agcaacagaa	tctcccatcc	agtccggcac	360
ccagtaccat	attctctgga	ggtttttagac	acggaagttt	aattagcatt	gacagcacct	420
gtacagagat	gggcaatttt	gacaatgcta	atgtcactgg	agaaatagaa	tttgccattc	480
attattgctt	caaaacccat	tctttagaaa	tatgcatcaa	ggcctgtaag	aaccttgctt	540
atggagaaga	aaagaagaaa	aagtgcattc	cgtatgtgaa	gacctacctg	ttgcccgcac	600
gatcctccca	gggaaagcgc	aagactggag	tccaaaggaa	caccgtggac	ccgacctttc	660
aggagacctt	gaagtatcag	gtggcccctg	cccagctggg	gacccggcag	ctgcaggtct	720
cgggtgtggca	tctgggcacg	ctggcccggg	gagtggtttc	tggaagaagt	atcatttcct	780

tggccacgtg	ggactttgaa	gacagcacia	cacagtcctt	ccgctggcat	ccgctccggg	840
ccaaggcgga	gaaatacgaa	gacagcggtc	ctcagagtaa	tggagagctc	acagtccggg	900
ctaagctggt	tctcccttca	cggcccagaa	aactccaaga	ggctcaagaa	gggacagatc	960
agccatcact	tcattgtcaa	ctttgtttgg	tagtgctagg	agccaagaat	ttacctgtgc	1020
ggccagatgg	caccttgaac	tcatttgtaa	agggctgtct	cactctgcca	gaccaacaaa	1080
aactgagact	gaagtcgcca	gtcctgagga	agcaggcttg	ccccagtg	aaacactcat	1140
ttgtcttcag	tggcgtaacc	ccagctcagc	tgaggcagtc	gagcttgag	ttactgtct	1200
gggatcaggc	cctctttgga	atgaacgacc	gcttgcttgg	aggaaccaga	cttggttcaa	1260
agggagacac	agctgtttgg	ggggatgcat	gctcacaatc	gaagctccag	tggcagaaa	1320
tcctttccag	ccccaatcta	tggacagaca	tgactcttgt	cctgcactga	catgaaggcc	1380
tcaaggttcc	aggttgagc	agggctgagg	cactgtgcgt	ctgcagaggg	gctacgaacc	1440
aggtgcaggg	tcccagctgg	agaccccttt	gaccttgagc	agtctccatc	tgcgccctg	1500
tcccatggct	taaccgccta	ttggtatctg	tgtatatatta	cgttaaacac	aattatgtta	1560
cctaagcctc	tgggtgggta	tctctctctt	gagatgtaga	aaatggccag	attttaataa	1620
acgttggttac	ccatgaaaaa	aaaaaaaa				1648

<210> 45
 <211> 313
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Delete: this sequence is a duplicate of Sequence 15

<400> 45
 Met Gly Asn Phe Asp Asn Ala Asn Val Thr Gly Glu Ile Glu Phe Ala
 1 5 10 15
 Ile His Tyr Cys Phe Lys Thr His Ser Leu Glu Ile Cys Ile Lys Ala
 20 25 30
 Cys Lys Asn Leu Ala Tyr Gly Glu Glu Lys Lys Lys Lys Cys Asn Pro
 35 40 45
 Tyr Val Lys Thr Tyr Leu Leu Pro Asp Arg Ser Ser Gln Gly Lys Arg
 50 55 60
 Lys Thr Gly Val Gln Arg Asn Thr Val Asp Pro Thr Phe Gln Glu Thr
 65 70 75 80
 Leu Lys Tyr Gln Val Ala Pro Ala Gln Leu Val Thr Arg Gln Leu Gln
 85 90 95
 Val Ser Val Trp His Leu Gly Thr Leu Ala Arg Arg Val Phe Leu Gly
 100 105 110
 Glu Val Ile Ile Pro Leu Ala Thr Trp Asp Phe Glu Asp Ser Thr Thr
 115 120 125
 Gln Ser Phe Arg Trp His Pro Leu Arg Ala Lys Ala Glu Lys Tyr Glu
 130 135 140
 Asp Ser Val Pro Gln Ser Asn Gly Glu Leu Thr Val Arg Ala Lys Leu
 145 150 155 160
 Val Leu Pro Ser Arg Pro Arg Lys Leu Gln Glu Ala Gln Glu Gly Thr
 165 170 175
 Asp Gln Pro Ser Leu His Gly Gln Leu Cys Leu Val Val Leu Gly Ala
 180 185 190
 Lys Asn Leu Pro Val Arg Pro Asp Gly Thr Leu Asn Ser Phe Val Lys
 195 200 205

Gly Cys Leu Thr Leu Pro Asp Gln Gln Lys Leu Arg Leu Lys Ser Pro
 210 215 220
 Val Leu Arg Lys Gln Ala Cys Pro Gln Trp Lys His Ser Phe Val Phe
 225 230 235 240
 Ser Gly Val Thr Pro Ala Gln Leu Arg Gln Ser Ser Leu Glu Leu Thr
 245 250 255
 Val Trp Asp Gln Ala Leu Phe Gly Met Asn Asp Arg Leu Leu Gly Gly
 260 265 270
 Thr Arg Leu Gly Ser Lys Gly Asp Thr Ala Val Gly Gly Asp Ala Cys
 275 280 285
 Ser Gln Ser Lys Leu Gln Trp Gln Lys Val Leu Ser Ser Pro Asn Leu
 290 295 300
 Trp Thr Asp Met Thr Leu Val Leu His
 305 310

<210> 46
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of the artificial sequence:oligonucleotide

<400> 46
 tcgtagagca gcaggtccaa g 21

<210> 47
 <211> 1945
 <212> DNA
 <213> Homo sapiens

<400> 47
 aatggaaggg cgtgagcgct tgggtccatgc agtgaagctc ttccaacctg ggtcaacgaa 60
 aacggagaag aaatggccca agaaatagat ctgagtgtctc tcaaggagtt agaacgcgag 120
 gccattctcc aggtcctgta ccgagaccag gcggttcaaa acacagagga ggagaggaca 180
 cggaactga aaacacacct gcagcatctc cgggtgaaag gagcgaagaa cacggactgg 240
 gagcaciaag agaagtgtgtg tgcgcgtgtc cagcaggtgc tgggggttcct gctgcaccgg 300
 ggcgccgtgt gccggggctg cagccaccgc gtgtgtgtccc agtgccgagt gttcctgagg 360
 gggacccatg cctggaagtg cacggtgtgtc ttcgaggaca ggaatgtcaa aataaaaact 420
 ggagaatggt tctatgagga acgagccaag aaatttccaa ctggaggcaa acatgagaca 480
 gttggagggc agctcttgca atcttatcag aagctgagca aaatttctgt ggttcctcct 540
 actccacctc ctgtcagcga gagccagtgc agccgcagtc ctggcagggtt acaggaattt 600
 ggtcagttta gaggatttaa taagtccgtg gaaaatttgt ttctgtctct tgctaccac 660
 gtgaaaaagc tctccaaatc ccagaatgat atgacttctg agaagcatct tctcgccacg 720
 Page 20

ggccccaggc agtgtgtggg acagacagag agacggagcc agtctgacac tgcggtcaac 780
 gtcaccacca ggaaggtcag tgcaccagat attctgaaac ctctcaatca agaggatccc 840
 aaatgtctcta ctaaccctat tttgaagcaa cagaatctcc catccagtcc ggcacccagt 900
 accatattct ctggaggttt tagacacgga agtttaatta gcattgacag cacctgtaca 960
 gagatgggca attttgacaa tgctaattgtc actggagaaa tagaatttgc cattcattat 1020
 tgcttcaaaa cccattcttt agaaatatgc atcaaggcct gtaagaacct tgcctatgga 1080
 gaagaaaaga agaaaaagtg caatccgtat gtgaagacct acctgttgcc cgacagatcc 1140
 tcccagggaa agcgcaagac tggagtccaa aggaacaccg tggacccgac ctttcaggag 1200
 accttgaagt atcagggtggc ccctgcccag ctggtgaccc ggcagctgca ggtctcggtg 1260
 tggcatctgg gcacgctggc ccggagagtg tttcttgagg aagtgatcat tcctctggcc 1320
 acgtgggact ttgaagacag cacaacacag tccttccgct ggcattccgct ccgggccaag 1380
 gcggagaaat acgaagacag cgttcctcag agtaatggag agctcacagt ccgggctaag 1440
 ctggtttctcc cttcacggcc cagaaaactc caagaggctc aagaagggac agatcagcca 1500
 tcacttcatt gtcaactttg tttggtagtg ctaggagcca agaatttacc tgtgcggcca 1560
 gatggcacct tgaactcatt tgttaagggc tgtctcactc tgccagacca acaaaaactg 1620
 agactgaagt cgccagtcct gaggaagcag gcttgccccc agtggaagaa ctcatttgtc 1680
 ttcagtggcg taaccccgag tcagctgagg cagtcgagct tggagttaac tgtctgggat 1740
 caggccctct ttggaatgaa cgaccgcttg cttggaggaa ccagacttgg ttcaaaggga 1800
 gacacagctg ttggcgggga tgcattgtca caatcgaagc tccagtggca gaaagtcctt 1860
 tccagcccca atctatggac agacatgact cttgtcctgc actgacatga aggcctcaag 1920
 gttccaggtt gcagcaggcg tgagg 1945

<210> 48
 <211> 610
 <212> PRT
 <213> Homo sapiens

<400> 48

Met Ala Gln Glu Ile Asp Leu Ser Ala Leu Lys Glu Leu Glu Arg Glu
 1 5 10 15

Ala Ile Leu Gln Val Leu Tyr Arg Asp Gln Ala Val Gln Asn Thr Glu
 20 25 30

Glu Glu Arg Thr Arg Lys Leu Lys Thr His Leu Gln His Leu Arg Trp
 35 40 45

Lys Gly Ala Lys Asn Thr Asp Trp Glu His Lys Glu Lys Cys Cys Ala
 Page 21

50

55

60

Arg Cys Gln Gln Val Leu Gly Phe Leu Leu His Arg Gly Ala Val Cys
65 70 75 80

Arg Gly Cys Ser His Arg Val Cys Ala Gln Cys Arg Val Phe Leu Arg
85 90 95

Gly Thr His Ala Trp Lys Cys Thr Val Cys Phe Glu Asp Arg Asn Val
100 105 110

Lys Ile Lys Thr Gly Glu Trp Phe Tyr Glu Glu Arg Ala Lys Lys Phe
115 120 125

Pro Thr Gly Gly Lys His Glu Thr Val Gly Gly Gln Leu Leu Gln Ser
130 135 140

Tyr Gln Lys Leu Ser Lys Ile Ser Val Val Pro Pro Thr Pro Pro Pro
145 150 155 160

Val Ser Glu Ser Gln Cys Ser Arg Ser Pro Gly Arg Leu Gln Glu Phe
165 170 175

Gly Gln Phe Arg Gly Phe Asn Lys Ser Val Glu Asn Leu Phe Leu Ser
180 185 190

Leu Ala Thr His Val Lys Lys Leu Ser Lys Ser Gln Asn Asp Met Thr
195 200 205

Ser Glu Lys His Leu Leu Ala Thr Gly Pro Arg Gln Cys Val Gly Gln
210 215 220

Thr Glu Arg Arg Ser Gln Ser Asp Thr Ala Val Asn Val Thr Thr Arg
225 230 235 240

Lys Val Ser Ala Pro Asp Ile Leu Lys Pro Leu Asn Gln Glu Asp Pro
245 250 255

Lys Cys Ser Thr Asn Pro Ile Leu Lys Gln Gln Asn Leu Pro Ser Ser
260 265 270

Pro Ala Pro Ser Thr Ile Phe Ser Gly Gly Phe Arg His Gly Ser Leu
275 280 285

Ile Ser Ile Asp Ser Thr Cys Thr Glu Met Gly Asn Phe Asp Asn Ala
290 295 300

Asn Val Thr Gly Glu Ile Glu Phe Ala Ile His Tyr Cys Phe Lys Thr

305					310						315					320
His	Ser	Leu	Glu	Ile	Cys	Ile	Lys	Ala	Cys	Lys	Asn	Leu	Ala	Tyr	Gly	
				325					330					335		
Glu	Glu	Lys	Lys	Lys	Lys	Cys	Asn	Pro	Tyr	Val	Lys	Thr	Tyr	Leu	Leu	
			340					345					350			
Pro	Asp	Arg	Ser	Ser	Gln	Gly	Lys	Arg	Lys	Thr	Gly	Val	Gln	Arg	Asn	
		355					360					365				
Thr	Val	Asp	Pro	Thr	Phe	Gln	Glu	Thr	Leu	Lys	Tyr	Gln	Val	Ala	Pro	
	370					375					380					
Ala	Gln	Leu	Val	Thr	Arg	Gln	Leu	Gln	Val	Ser	Val	Trp	His	Leu	Gly	
385					390					395					400	
Thr	Leu	Ala	Arg	Arg	Val	Phe	Leu	Gly	Glu	Val	Ile	Ile	Pro	Leu	Ala	
				405					410					415		
Thr	Trp	Asp	Phe	Glu	Asp	Ser	Thr	Thr	Gln	Ser	Phe	Arg	Trp	His	Pro	
			420					425					430			
Leu	Arg	Ala	Lys	Ala	Glu	Lys	Tyr	Glu	Asp	Ser	Val	Pro	Gln	Ser	Asn	
		435					440					445				
Gly	Glu	Leu	Thr	Val	Arg	Ala	Lys	Leu	Val	Leu	Pro	Ser	Arg	Pro	Arg	
	450					455					460					
Lys	Leu	Gln	Glu	Ala	Gln	Glu	Gly	Thr	Asp	Gln	Pro	Ser	Leu	His	Gly	
465					470					475					480	
Gln	Leu	Cys	Leu	Val	Val	Leu	Gly	Ala	Lys	Asn	Leu	Pro	Val	Arg	Pro	
				485					490					495		
Asp	Gly	Thr	Leu	Asn	Ser	Phe	Val	Lys	Gly	Cys	Leu	Thr	Leu	Pro	Asp	
			500					505					510			
Gln	Gln	Lys	Leu	Arg	Leu	Lys	Ser	Pro	Val	Leu	Arg	Lys	Gln	Ala	Cys	
		515					520					525				
Pro	Gln	Trp	Lys	His	Ser	Phe	Val	Phe	Ser	Gly	Val	Thr	Pro	Ala	Gln	
	530					535					540					
Leu	Arg	Gln	Ser	Ser	Leu	Glu	Leu	Thr	Val	Trp	Asp	Gln	Ala	Leu	Phe	
545					550					555					560	
Gly	Met	Asn	Asp	Arg	Leu	Leu	Gly	Gly	Thr	Arg	Leu	Gly	Ser	Lys	Gly	

565

570

575

Asp Thr Ala Val Gly Gly Asp Ala Cys Ser Gln Ser Lys Leu Gln Trp
 580 585 590

Gln Lys Val Leu Ser Ser Pro Asn Leu Trp Thr Asp Met Thr Leu Val
 595 600 605

Leu His
 610

<210> 49
 <211> 1741
 <212> DNA
 <213> Homo sapiens

<400> 49
 aatggaaggg cgtgagcgct tgggtccatgc agtgaagctc ttccaacctg ggtcaacgaa 60
 aacggagaag aaatggccca agaaatagat ctgagtgtctc tcaaggagtt agaacgcgag 120
 gccattctcc aggtcctgta ccgagaccag gcggttcaaa acacagagga ggagaggaca 180
 cggaaactga aaacacacct gcagcatctc cgggtggaag gagcgaagaa cacggactgg 240
 gagcaciaag agaagtgtctg tgcgcgctgc cagcaggtgc tgggggttcct gctgcaccgg 300
 ggcgcctgtg gccggggctg cagccaccgc gtgtgtgtccc agtgccgagt gttcctgagg 360
 gggacccatg cctggaagtg cacggtgtgc ttcgaggaca ggaatgtcaa aataaaaact 420
 ggagaatggt tctatgagga acgagccaag aaattttcaa ctggaggcaa acatgagaca 480
 gttggagggc agctcttgca atcttatcag aagctgagca aaatttctgt ggttcctcct 540
 actccacctc ctgtcagcga gagccagtgc agccgcagtc ctggcaggaa ggtcagtgc 600
 ccagatatcc tgaaacctct caatcaagag gatcccaaat gctctactaa ccctattttg 660
 aagcaacaga atctcccatc cagtccggca cccagtacca tattctcttg aggttttaga 720
 cacggaagtt taattagcat tgacagcacc tgtacagaga tgggcaattt tgacaatgct 780
 aatgtcactg gagaaataga atttgccatt cattattgct tcaaaaccca ttcttttagaa 840
 atatgcatca aggcctgtaa gaaccttgcc tatggagaag aaaagaagaa aaagtgcatt 900
 ccgtatgtga agacctacct gttgcccgcac agatcctccc agggaaagcg caagactgga 960
 gtccaaagga acaccgtgga cccgaccttt caggagacct tgaagtatca ggtggcccct 1020
 gccagctgg tgacccggca gctgcaggtc tcggtgtggc atctgggcac gctggcccgg 1080
 agagtgtttc ttggagaagt gatcattcct ctggccacgt gggactttga agacagcaca 1140
 acacagtcct tccgctggca tccgctccgg gccaaaggcg agaaatacga agacagcggt 1200
 cctcagagta atggagagct cacagtccgg gctaagctgg ttctcccttc acggcccaga 1260
 aaactccaag aggtcaaga agggacagat cagccatcac ttcattgtca actttgtttg 1320

gtagtgctag gagccaagaa ttacctgtg cgccagatg gcacctgaa ctcatgtt 1380
 aagggctgtc tctctgtcc agaccaaaa aaactgagac tgaagtcgcc agtcctgagg 1440
 aagcaggctt gccccagtg gaaacactca ttgtcttca gtggcgtaac ccagctcag 1500
 ctgaggcagt cgagcttga gttaactgtc tgggatcagg ccctcttgg aatgaacgac 1560
 cgcttgcttg gaggaaccag acttggttca aaggagaca cagctgttgg cgggatgca 1620
 tgctcacaat cgaagctcca gtggcagaaa gtcctttcca gcccattct atggacagac 1680
 atgactcttg tctgtcactg acatgaaggc ctcaagggtc cagggttcag caggcgtgag 1740
 g 1741

<210> 50
 <211> 542
 <212> PRT
 <213> Homo sapiens
 <400> 50

Met Ala Gln Glu Ile Asp Leu Ser Ala Leu Lys Glu Leu Glu Arg Glu
 1 5 10 15

Ala Ile Leu Gln Val Leu Tyr Arg Asp Gln Ala Val Gln Asn Thr Glu
 20 25 30

Glu Glu Arg Thr Arg Lys Leu Lys Thr His Leu Gln His Leu Arg Trp
 35 40 45

Lys Gly Ala Lys Asn Thr Asp Trp Glu His Lys Glu Lys Cys Cys Ala
 50 55 60

Arg Cys Gln Gln Val Leu Gly Phe Leu Leu His Arg Gly Ala Val Cys
 65 70 75 80

Arg Gly Cys Ser His Arg Val Cys Ala Gln Cys Arg Val Phe Leu Arg
 85 90 95

Gly Thr His Ala Trp Lys Cys Thr Val Cys Phe Glu Asp Arg Asn Val
 100 105 110

Lys Ile Lys Thr Gly Glu Trp Phe Tyr Glu Glu Arg Ala Lys Lys Phe
 115 120 125

Pro Thr Gly Gly Lys His Glu Thr Val Gly Gly Gln Leu Leu Gln Ser
 130 135 140

Tyr Gln Lys Leu Ser Lys Ile Ser Val Val Pro Pro Thr Pro Pro Pro
 145 150 155 160

Val Ser Glu Ser Gln Cys Ser Arg Ser Pro Gly Arg Lys Val Ser Ala
165 170 175
Pro Asp Ile Leu Lys Pro Leu Asn Gln Glu Asp Pro Lys Cys Ser Thr
180 185 190
Asn Pro Ile Leu Lys Gln Gln Asn Leu Pro Ser Ser Pro Ala Pro Ser
195 200 205
Thr Ile Phe Ser Gly Gly Phe Arg His Gly Ser Leu Ile Ser Ile Asp
210 215 220
Ser Thr Cys Thr Glu Met Gly Asn Phe Asp Asn Ala Asn Val Thr Gly
225 230 235 240
Glu Ile Glu Phe Ala Ile His Tyr Cys Phe Lys Thr His Ser Leu Glu
245 250 255
Ile Cys Ile Lys Ala Cys Lys Asn Leu Ala Tyr Gly Glu Glu Lys Lys
260 265 270
Lys Lys Cys Asn Pro Tyr Val Lys Thr Tyr Leu Leu Pro Asp Arg Ser
275 280 285
Ser Gln Gly Lys Arg Lys Thr Gly Val Gln Arg Asn Thr Val Asp Pro
290 295 300
Thr Phe Gln Glu Thr Leu Lys Tyr Gln Val Ala Pro Ala Gln Leu Val
305 310 315 320
Thr Arg Gln Leu Gln Val Ser Val Trp His Leu Gly Thr Leu Ala Arg
325 330 335
Arg Val Phe Leu Gly Glu Val Ile Ile Pro Leu Ala Thr Trp Asp Phe
340 345 350
Glu Asp Ser Thr Thr Gln Ser Phe Arg Trp His Pro Leu Arg Ala Lys
355 360 365
Ala Glu Lys Tyr Glu Asp Ser Val Pro Gln Ser Asn Gly Glu Leu Thr
370 375 380
Val Arg Ala Lys Leu Val Leu Pro Ser Arg Pro Arg Lys Leu Gln Glu
385 390 395 400
Ala Gln Glu Gly Thr Asp Gln Pro Ser Leu His Gly Gln Leu Cys Leu
405 410 415

Val Val Leu Gly Ala Lys Asn Leu Pro Val Arg Pro Asp Gly Thr Leu
420 425 430

Asn Ser Phe Val Lys Gly Cys Leu Thr Leu Pro Asp Gln Gln Lys Leu
435 440 445

Arg Leu Lys Ser Pro Val Leu Arg Lys Gln Ala Cys Pro Gln Trp Lys
450 455 460

His Ser Phe Val Phe Ser Gly Val Thr Pro Ala Gln Leu Arg Gln Ser
465 470 475 480

Ser Leu Glu Leu Thr Val Trp Asp Gln Ala Leu Phe Gly Met Asn Asp
485 490 495

Arg Leu Leu Gly Gly Thr Arg Leu Gly Ser Lys Gly Asp Thr Ala Val
500 505 510

Gly Gly Asp Ala Cys Ser Gln Ser Lys Leu Gln Trp Gln Lys Val Leu
515 520 525

Ser Ser Pro Asn Leu Trp Thr Asp Met Thr Leu Val Leu His
530 535 540